```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298A97;
                                                                                                                                                                                                            O7UOE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q98A97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
Q98A97
                                                                                                                                                                                        RESULT 1
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RXCOCCUENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q82cw2 streptomyce
Q97km5 streptomyce
Q97km5 streptomyce
Q97ku4 mnopheles g
Q77ku5 neurospora
Q864m6 mus musculu
Q87xn5 ralstonia s
Q9988 phaeosphaer
Q67kd2 gallid herp
Aa948543 gallid herp
Aa948543 gallid herp
Aa109767 gallid herp
Q81059 streptomyce
Q67642 gallid herp
P53535 solanum tub
Q6653 gallid herp
P65535 fundulus her
Q86457 fundulus he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7zyk8 xenopus lae
Q64541 rattus norv
Q9kie9 streptomyce
Q9nex6 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                  Q98a97 rhizobium l
Q8kjf9 rhizobium l
Q7qc63 anopheles g
                                                                                                                                                                                                                                                                                                                                                                                                                         Q7uqe4 rhodopirell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aaq82787 oncorhync
P05025 torpedo cal
                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                               January 31, 2005, 18:02:30; Search time 148.167 Seconds (without alignments) 54.366 Million cell updates/sec
                                                                                                                                                                                                  1825181
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                             1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07RUAS
08C4M6
08RC4M6
06RXZNS
06RXZNS
09P858
06PL14
AAS48543
AAS48543
AAS48543
AAT09767
09F042
067642
09F052
PRS2 SOLTU
06B126
08653
AAQ82787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATIA TORCA
A1AI HUMAN
Q7ZYK8
A1A4 RAT
Q9KIE9
                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                        07U0E4
09BA97
08KJF9
07QC63
082CW2
09RKM5
                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                     UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                            CADGPTLREWISFC 14
                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
                                                                                                        US-10-083-768-12
85
                                                                                                                                                                                                                                                                                                                                                                                                     Length DB
                                                                                                                                                                                                                                                                                                                                                                                         Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                50.5
50.5
48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                             OM protein
                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                                                                                             Sequence:
                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                         Database
                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                          Result
```

```
ö
                 Q8hyw6 bos taurus Q866a9 equus cabal Q9m060 arabidopsis Q6nmu4 drosophila Q9x55 drosophila Aaa15697 drosophila Q37839 bacteriopha Q8b129 mus musculu Q80149 mus musculu Q71419 homo sapien Q98s13 electrophor
   oryctolaque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBL TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome; Hypothetical protein.
SEQUENCE 297 AA; 31805 MW; 475F670F02C78E9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl, Acad. Sci. U.S.A. 100:8298-8303(2003)
EMBL; BX294144; CAD74759.1;
InterPro; IPR001194; ATPASe_a/bcentre.
InterPro; IPR003169; GYF
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
PROSITE; PS50829; GYF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.4%; Score 53; DB 2; 72.7%; Pred. No. 1.1; ive 3; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                    297 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 AA
                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                Q866A9
Q9M060
Q6MW14
Q9VKS5
AAS15697
Q37839
Q01789
Q80UZ8
Q91YY9
Q98L13
                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22735913; PubMed=12835416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2001 (TrEMBLrel. 18, 01-0CT-2001 (TrEMBLrel. 18, 01-0CT-2003 (TrEMBLrel. 24, Mlr6096 protein. 0rderedLocusNames=mlr6096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=RB6375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 72.7
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||:::|||
175 ADGPTMKQWIS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
1127
1171
1176
2245
2465
4607
4607
469
600
960
960
960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodopirellula baltica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ADGPTLREWIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=117;
```

```
EMBL; AAABO1008859; EAA08177.1; -.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004672; F:ATP binding; IEA.

R GO; GO:0004672; F:protein Kinase activity; IEA.

R GO; GO:0016740; F:protein kinase activity; IEA.

R GO; GO:0016740; F:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR001726; S methyl trans.

R Pfam; PF00069; Pkinase; 1.

R Pfam; PF00069; Pkinase; 1.

R Propom; PD000001; Prot Kinase; 1.

R Propom; PD000001; Prot Kinase; 1.

R PROPOM; PSS0011; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles Genome Sequencing Consortium;
Submitted (MAK-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; Gequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bactèria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB 2; Length 1123;
Pred. No. 34;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QB2CW2 PRELIMINARY; PRT; 283 AA.
OB2CW2;
OB1JUN-2003 (TrEMBLrel. 24, Created)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                  01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolites.";
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative IcIR-family transcriptional regulator.
OrderedLocusNames=SAV5226;
                                                                                                                                                                                                                                                                                                                                                AgCP1221.
Name=agCG53078; ORFNames=ENSANGG0000018866;
                                                                                                                                                                                      PRT; 1123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21477403; PubMed=11572948;
243 CADGKEVIFSVQNDREWVNFC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           969 ADHPTVRFWISF 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ADGPTLREWISF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces avermitilis
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MA-4680;
                                                                                                                                                                                                                                                  01-MAR-2004
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                         Q7QC63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPART TERMS OF SERVICE SERVIC
                                                                                                                             RESULT
Q7QC63
                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                           Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kibida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., "Complete genome structure of the itrogen-fixing symbiotic bacterium Mesorhizobium loti (supplement).";

SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDITARE 1797.7.7 Trzebiatowski J.R., Cruickshank R.W., Gouzy J., Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U., Stuliar G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.W.; "Comparative sequence analysis of the symbiosis island of Wesorhizobium loti strain R7A."; J. Bacteriol. 184:3086-3095 (2002).

GO, GO:0008152; P:metabolism; IEA.
InterPro; IRF003673; CAB_BAIF.
Frank, PF02515; CAA transf 3; 1.
SEQUENCE 389 AA; 42703 MW; 6678D2C96A7E5204 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 AA; 42226 MW; 64643EBEC8F25518 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.4%; Score 50.5; L
42.9%; Pred. No. 4;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.4%; Score 50.5; 42.9%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUTATIVE RACEMASE/DEHYDRATASE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21999272; PubMed=12003951;
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 CADGKEVIFSVQNDREWVNFC 257
                                            STRAIN=MAFF303099;
MEDLINE=21082936; PubMed=11214974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 7:331-338(2000).
EMBL, AP003008; BAB52440.1; -.
GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CADGPTL-----REWISFC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CADGPTL-----REWISFC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003673; CAIB BAIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02515; COA_transf_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Query Match
Best Local Similarity 42.>,,
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome
SEQUENCE 387 AA
                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=381;
```

OBKJF9 Q8KJF9

RESULT 3

8 셤 ö

Gaps

ö

```
Q7PPP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7RUA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                  엄
                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                 Η;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                       Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitlis.";
Mat. Biotechnol. 21:526-531(2003).
EMBL; APO05042; BAC72938.1;
GO; GO:0003577; F:DNA binding; IEA.

GO; GO:0003577; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K.W., Ruter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BMEL, AL939118; CAB56383.1; -..
GO; GO:0005622; Cintracellular; IEA.
GO; GO:0005509; Cintracellular; IEA.
GO; GO:000535; F:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000551; HTH MerR.
InterPro; IPR009061; Putativ_DNA_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                 55.9%; Score 47.5; DB 2; Length 283; 50.0%; Pred. No. 9.4; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.1%; Score 46; DB 2; Length 319; 70.0%; Pred. No. 20; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00422; HTH MERR; 1.
PROSITE; PS50937; HTH MERR 2; 1.
Complete proteome; DNĀ-binding.
SEQUENCE 319 AA; 34841 MW; 1F51905A8BA5365E CRC64;
                                                                                                                                                                                                                      283 AA; 30503 MW; F63B1705578EEE67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative MerR family transcriptional regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OrderedLocusNames=SCO4102; ORFNames=SCD17.06c;
                                                                                                                                                                                                                                                                                                                                                                                                                 319 AA
                                                                                                                                                         Interpro; IPR005471; HTH ICIR.
Interpro; IPR009058; Wing_hlx_DNA_bnd
Pfam; PF01614; ICIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
             STRAIN=MA-4680;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                           ||:||| : ||: |
152 CAEGPTTPAVHEWVDF 167
                                                                                                                                                                                                                                                                                                           1 CADGPT---LREWISF 13
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0°
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00040; HTHMERR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.0.
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                        Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hopwood D.A.;
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9RKM5;
                                                                                                                                                                                                                                                                                                                                                                                                                O9RKM5
                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
Q9RKM5
ò
                                                                                                                                                                                                                                                                                                                                     名
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A dalagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Bitlins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., A Dui D., Ianakiev P., Redersen D., Nelson M., Washburne M., Schulte U., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysselis M., Maucell E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seller S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Pullsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.; Nature O:0-0(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                          Name-ENSANGG00000018280;
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0008898; F:homocysteine S-methyltransferase activity; IEA. InterPro; IRR03726; S.methyl trans. PF02574; S-methyl trans. NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles Genome Sequencing Consortium,
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 347 AA; 38585 MW; 66FF58A1000CDA4F CRC64;
                                                                                                                                                                                  01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.1%; Score 46; DB 61.5%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary data.
EMBL; AAAB01008944; EAA10075.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004 (TrEMBLrel. 26, Cres
01-MAR-2004 (TrEMBLrel. 26, Last
01-MAR-2004 (TrEMBLrel. 25, Last
Hypothetical protein B24819.30.
                                                                                                                                                                                                                                                      ENSANGP0000020769 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 CDEYPTVRFWISF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CADGPTLREWISF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
258 DGPELREWLA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=OR74A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=NCU03933.1
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=PEST
```

```
CAE29718
CAE29718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06N1X5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAE29718
ID CAE2
AC CAE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAN PRESENTANT OF SERVICE OF SERV
   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=GSPBL/61; ITSUE=Head;
MEDLINE=20499374; PubMed=11042159;
Carrinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Shibata to
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=2530913; PubMed=11076861;
MEDLINE=2530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OL-MAR-2003 (TrEMBLrel. 23, Created)
Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update).
Ol-MUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1011_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21085660; PubMed=11217851;
MENTEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                Score 45; DB 2; Length 108;
Pred. No. 9.1;
2; Mismatches 5; Indels
                                                        preliminary data.
EMBL; AABXO1000719; EAA28336.1; -.
Hypochetical protein.
SEQUENCE 108 AA; 11994 MW; 093DC0D9617A252E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
                                                                                                                                                                                                                      52.9%;
                                                                                                                                                                                                                                                                                                                                                       1 CADGPTLREWISFC 14
                                                                                                                                                                                                                                                                                                                                                                                                                   70 ĆQCQPILRNWLSWC 83
                                                                                                                                                                                                                                                       Local Similarity 50.0 nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=C130070B15Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sednence.
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8C4M6
Q8C4M6;
                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9

ORC4M6

ORC4M6

ORC4M6

ORC4M6

ORC4M6

ORC4M1

ORC4M8

ORC4M8

ORC6M8

ORC6
   SSSSSS
                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hayashida K., Ishii Y., Itoh M., Kagawa I., Kaukawa T.,
Katoh H., Kawai J., Kojima Y., Kono H., Kouda M., Koya S.,
Katoh H., Kawai J., Kojima Y., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saitoh H., Sata C., Sakazume N., Sano H.,
Sasaki D., Saitoh H., Sakai C., Sakazume N., Sano H.,
Asasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, MGI:2444974; C130070815Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=14704707, DOI=10.1038/nbt923;
PubMed=14704707, DOI=10.1038/nbt923;
PubMed=14704707, DOI=10.1038/nbt923;
PubMed=14704707, DOI=10.1038/nbt923;
Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L., Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., Harrison F.H., Gibson J., Harvaod C.S., "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";
Nat. Biotechnol. 22:55-61 (2004).
EmBL, BXS72606; CAE29718.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.9%; Score 45; DB 2; Length 173; 63.6%; Pred. No. 15; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 AA; 23238 MW; 6FE082A84DB040EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19340 MW; 6227DD6725E52FCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteome; Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CADTGYEAALPTIREWLS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CADG-----PTLREWIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodopseudomonas palustris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
OrderedLocusNames=RPA4277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GPTLREWISFC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 GVTMŘEŇAŠWĆ 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004
```

i,

ö

```
1 CADGPTLREWISFC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 CSENGTLREWIT 181
                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CADGPTLREWIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                             221 CTDGAVLREW 230
                             1 CADGPTLREW 10
                                                                                                                                                                                                                                                                                        Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10386;
                                                                                                                                                                                                                                                                                                                                        Plasmid pElsal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BS444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BS444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rawson J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6QHD2;
                                                                                                                                                                             Q9P858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            060HD2
                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                  g
                                                                                                                                                                                                      ACCOCCOS SELECTED SELECTES SEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                 Larimer F.W., Chain P., Hauser L., Lamerdin J., Malfatti S., Do L., Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobbt C., Torres y Torres J.L., Peres C., "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris."; Nat. Biotechnol. 22:55-61(2004).

EMBL, BX572606; CAE29718.1; -.

Hypothetical protein.

SEQUENCE 209 AA; 23238 MW; 6FE082A84DB040EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Frenard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siquier P., Thebault P., Whalen M., Wincker P., Levy M., Meissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL646664, CAD15062.1; -. GO, GO, 60003700; Fitranscription factor activity; IEA. GO; GO:0006135; P:regulation of transcription, DNA-dependent; IEA. InterPro; IPR00644; HTH LysR. InterPro; IPR005119; LysR. subst. InterPro; IPR00518; Wing_hlx_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PROBABLE TRANSCRIPTION REGULATOR PROTEIN.
Name=RS04642; OrderedLocusNames=RSc1360;
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiaceae; Ralstonia.
                                                                                                           Rhodopseudomonas palustris.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Rhodopseudomonas.
NCBI_TaxID=1076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 2; Length 209;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.9%; Score 45; DB 2; Length 309; 70.0%; Pred. No. 28; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  733551741CE83182 CRC64;
  (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-GM11000;
MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  substrate; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 CADTGYEAALPTIREWLS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CADG-----PILREWIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 309 AA; 33774 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50931; HTH LYSR; 1.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CGA009 / ATCC BAA-98;
PubMed=14704707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.9%;
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.9
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00126; HTH 1; 1
Pfam; PF03466; LysR sub
                                                                  Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBXZNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
                                                                                                                                                                                                                                                                                                                                                                                                      "Transposable elements in the phytopathogenic fungus Stagonospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                          Eukaryota, Fungi, Ascomycota, Pezizomycotina, Dothideomycetes,
Pleosporales, Phaeosphaeriaceae, Phaeosphaeria.
NCBI_TaxID=13684,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P32 (Fragment).
Gallid herpesvirus 1.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Villarreal L.Y., Brandao P.E., Ferreira A.P., Doretto L.J., D'elboux A.N.;
Submitted (B.E.2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY541676; AAS48543.1; -.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rawson J.M., Cutler S.B., Caten C.E.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ277966; CAB91876.1; -1
Hypothetical protein: Plasmid.
SEQUENCE 443 AA; 49466 WW; 367E0762EE839FAR CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thesis (2000), PhD thesis, University of Birmingham, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 AA; 19130 MW; 5AE4A1956CEB9B13 CRC64;
                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.9%; Score 45; DB 2; 58.3%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.8%; Score 44; DB 2; 50.0%; Pred. No. 23;
443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                          Phaeosphaeria nodorum (Septoria nodorum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
PRT;
```

ô

ö

120 CLDMPPLRPWTTVC 133

d

```
RESULT 15
AAS48543
ID AAS48543
ID AAS48543
ID AAS48543
ID AAS48543

AC AAS48543

DT 10-WAR-2004 (TrEMBLrel. 27, Created)
DT 10-WAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-WAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-WAR-2004 (TrEMBLrel. 27, Last annotation update)
DT 10-WAR-2004 (TrEMBLrel. 27, Last annotation update)
OC Gallid herpesvirinas;
OC Viruses; dsDNA viruses.
OC Viruses; dsDNA viruses.
OC Alphaherpesvirinae; Infectious larymgotracheitis-like viruses.
OC Alphaherpesvirinae; Infectious larymgotracheitis-like viruses.
NCBI_TAXID=10386;
RN [1]
RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RP Villarreal L.Y., Brandao P.E., Ferreira A.P., Doretto L.J.,
RA Villarreal L.Y., Brandao P.E., Ferreira A.P., Doretto L.J.,
RA D'elboux A.N.;
D'elboux A.N.;
RY "Molecular epidemiology of an outbreak of infectious larymgotracheitis
RT "Molecular epidemiology of an outbreak of infectious larymgotracheitis
RT "Molecular epidemiology of an outbreak of infectious larymgotracheitis
RT "MON TER 173 AAS48543.1; -
FT NON TER 173 AAS 19130 NW; SAE4A19S6CEB9B13 CRC64;
Ouery Match
Best Local Similarity 50.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
```

Search completed: January 31, 2005, 18:21:43 Job time: 151.167 secs

120 CLDMPPLRPWTTVC 133

1 CADGPTLREWISFC 14

දු පු